Identifier les scénarios complexes de colonisation à l'échelle continentale des champignons pathogènes à l'aide des méthodes ABC

Benoit Barrès[1,2,3], Stéphanie Robert[2], Catherine Abadie[2], Jean Carlier[2], Cyril Dutech[1] et Virginie Ravigné[2]

[1] UMR BIOGECO [2] UMR BGPI [3] UPR 31

Why reconstruct routes of emergences ?

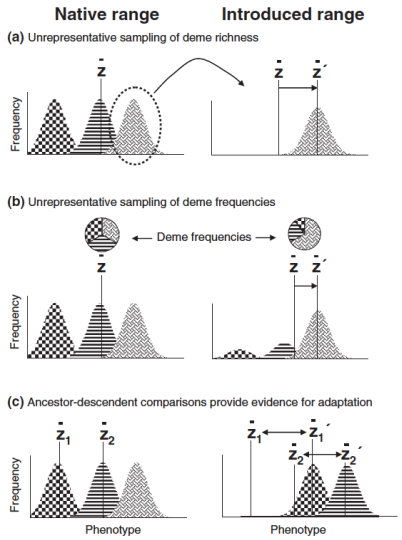
-Identify source populations

-Gain insights on dispersal mode

-Understand the process involved in emergence (admixture, bridgehead effect)

➔Improve quarantine politics

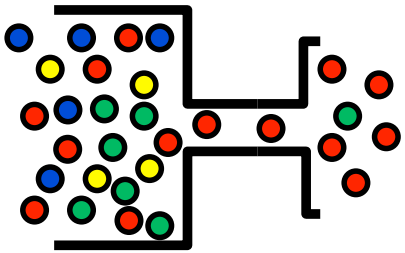
➔First step in the identification of evolutionary changes linked with emergence (comparison between source populations and emerging populations)



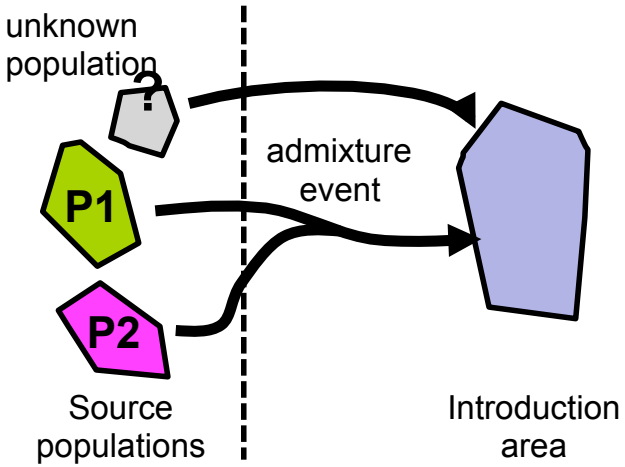
(Keller and Taylor, 2008)

Why use ABC methods ?

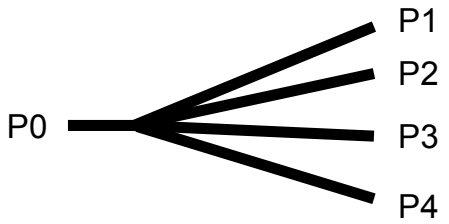
Demographic variation



Source population identification



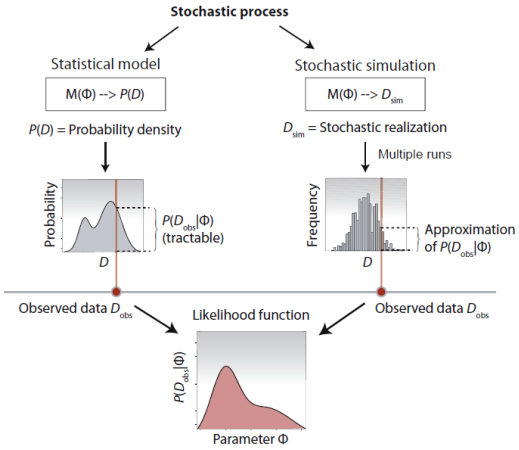
Multifurcation



-Assignment methodology (GeneClass2)
-Model-based coalescent method (MIGRATE, IM, …)

➔Need tractable Likelihoods

…but Likelihoods are not always tractable



(Hartig *et al.*, 2011)

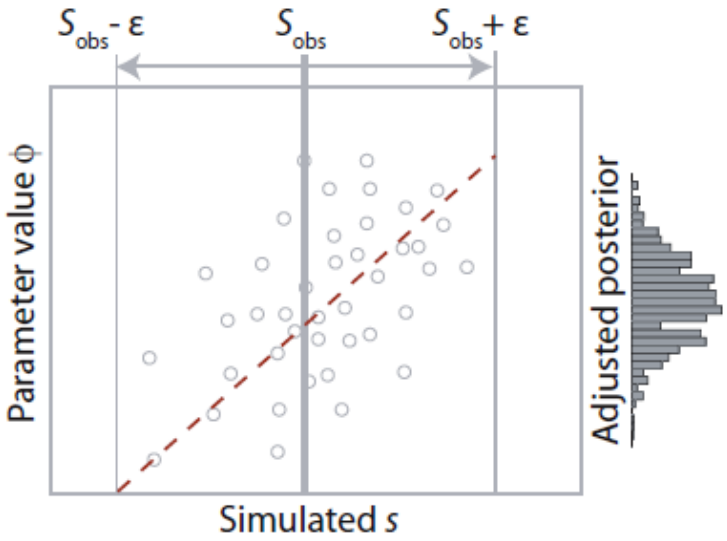
The ABC framework

3 steps :

1) generating (a lot of) simulated data sets

2) selecting simulated data sets closest to observed data set

3) estimating posterior distributions of parameters through a regression procedure



(*Excoffier et al.*, 2005)

(Hartig *et al.*, 2011)

Reviews: Beaumont 2010; Bertorelle *et al.*, 2010; Csilléry *et al.*, 2010

DIYABC software

-design and simulation of scenarios
(admixture, unsampled population, divergence between populations)

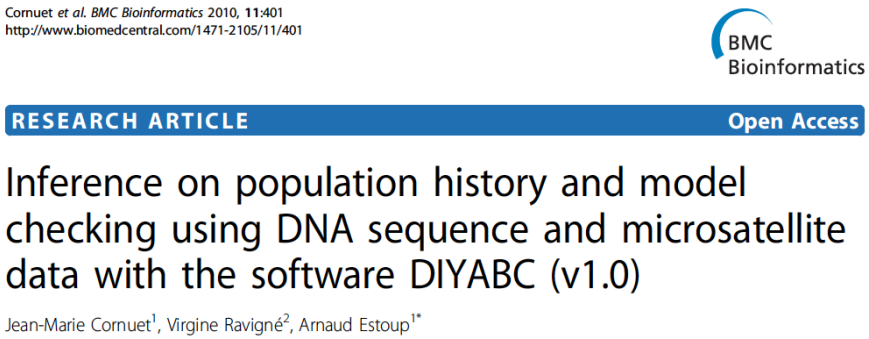
-tools to perform tests on priors distribution

-evaluation of posterior distribution

-tools to assess confidence and goodness of fit of the model

-haploid and diploid data

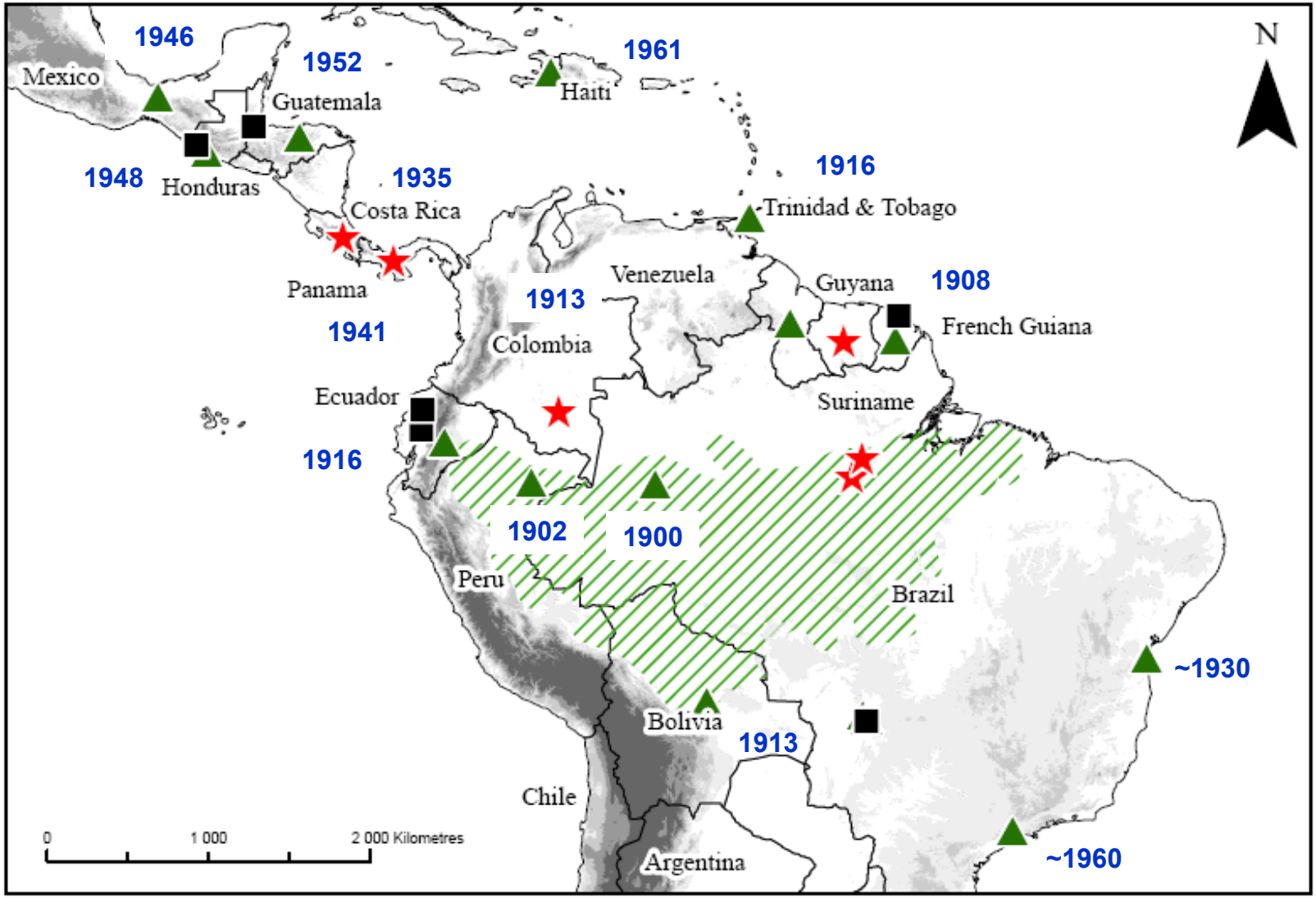
-microsatellite and/or sequence data



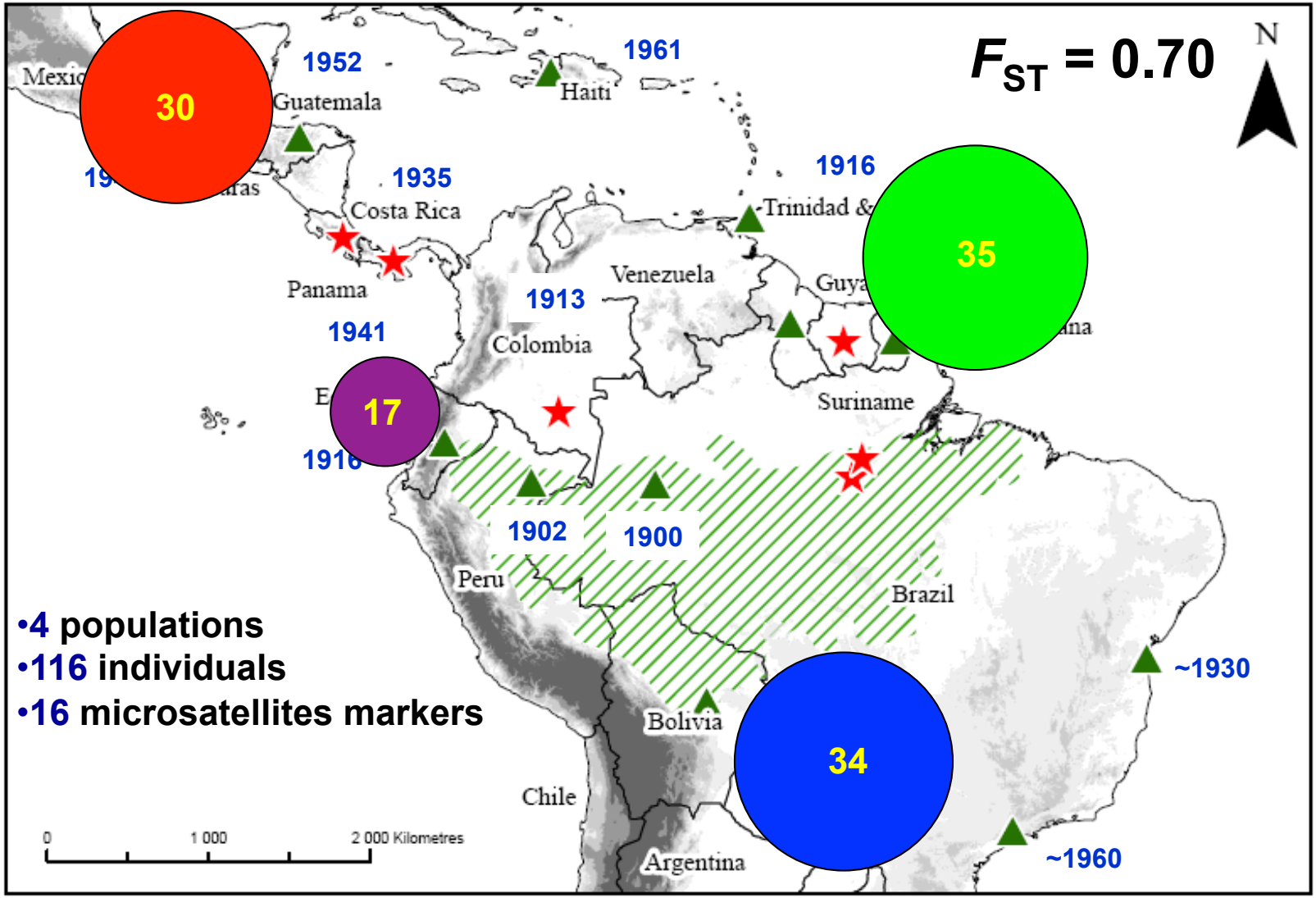
Continental scale dispersal of *Microcyclus ulei*

Benoit Barrès, Jean Carlier, Marc Seguin, Catherine Fenouillet, Christian Cilas and Virginie Ravigné

Continental scale dispersal of *Microcyclus ulei*

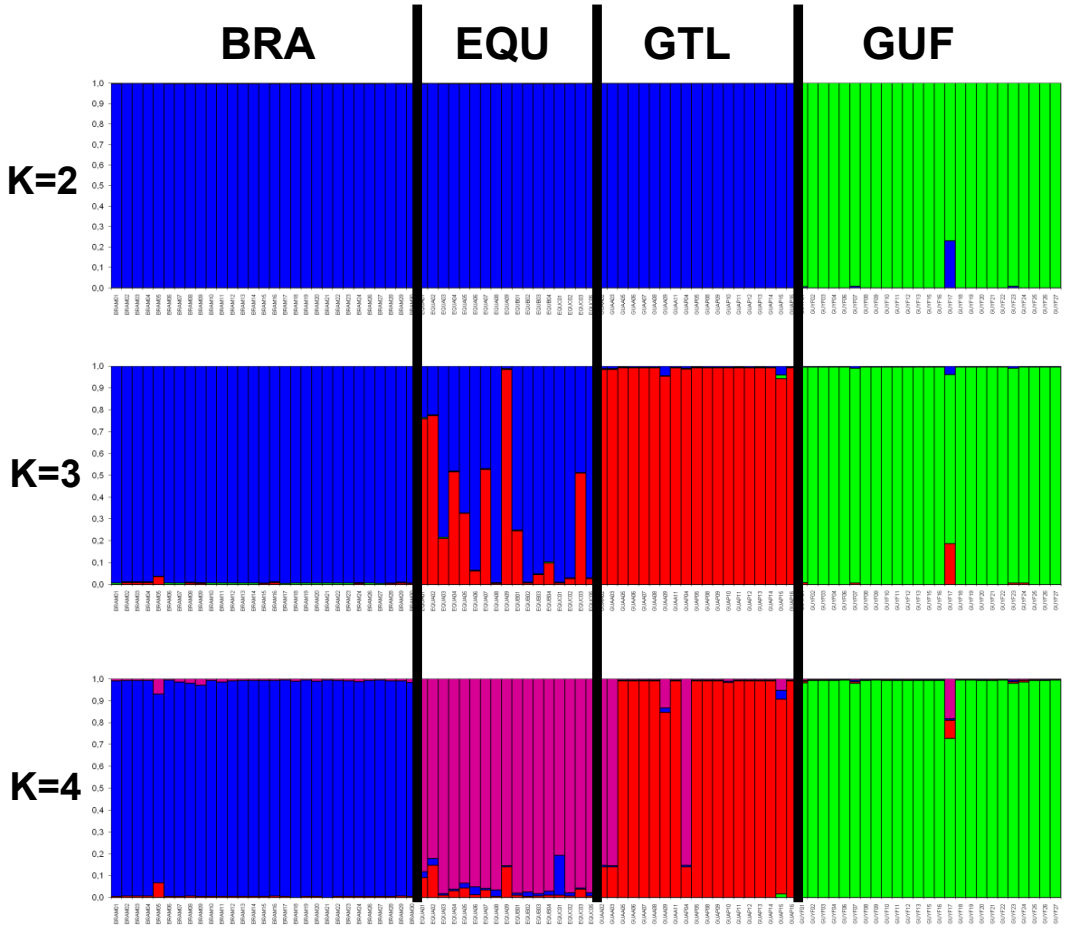


Sampling design

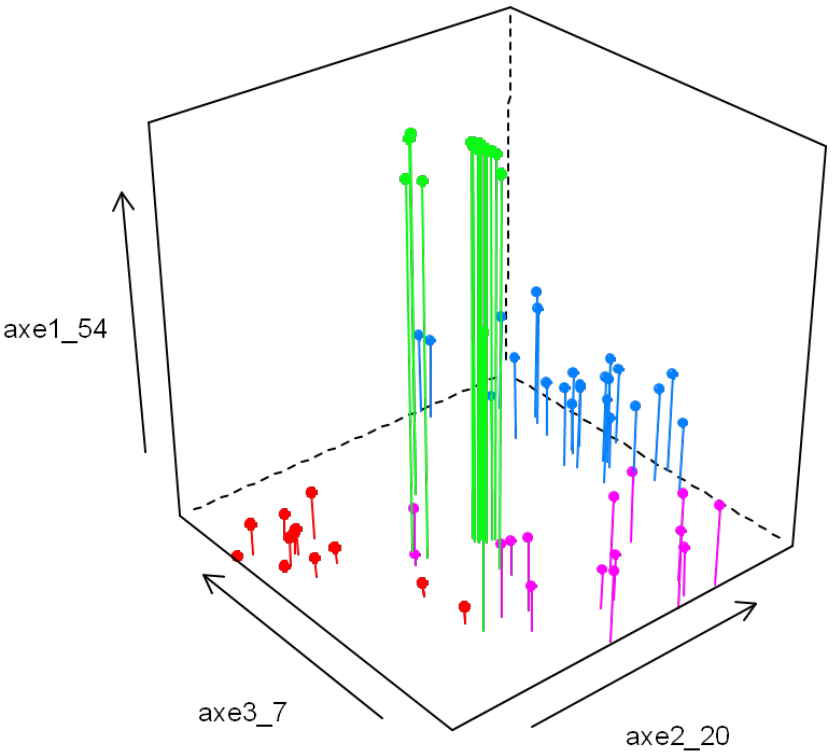


Genetic structure

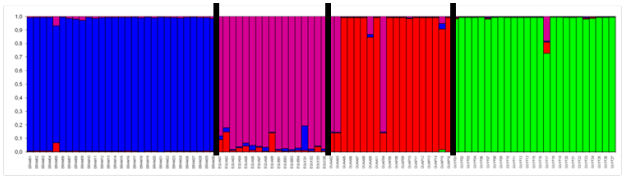
Bayesian Clustering

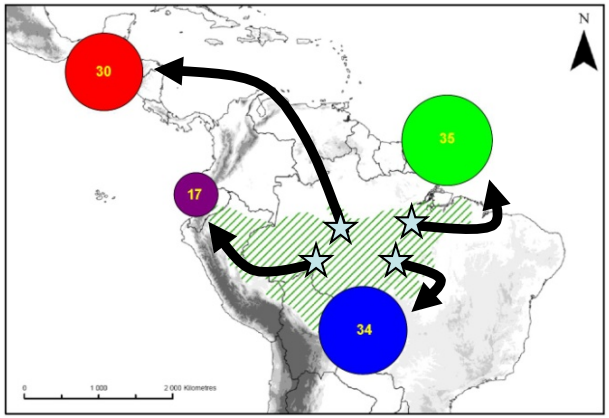


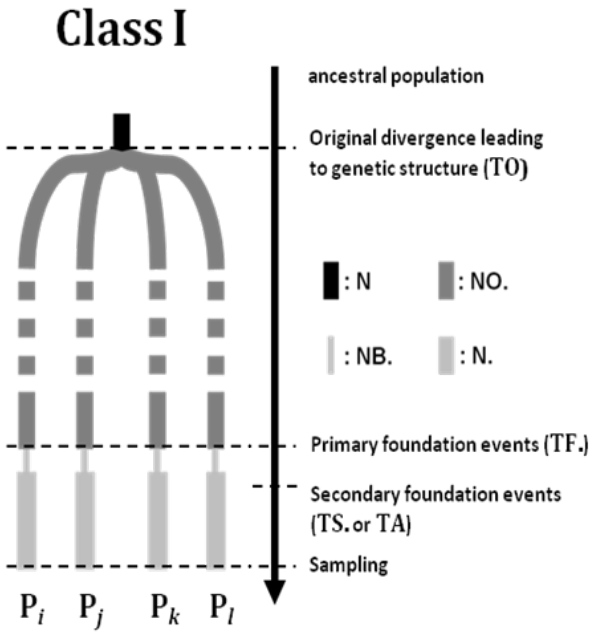
PCA



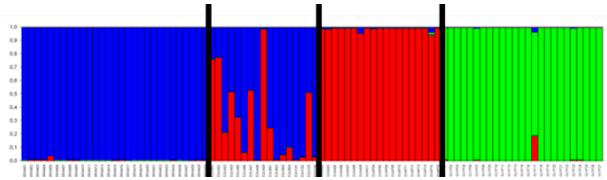
Four independent foundation events

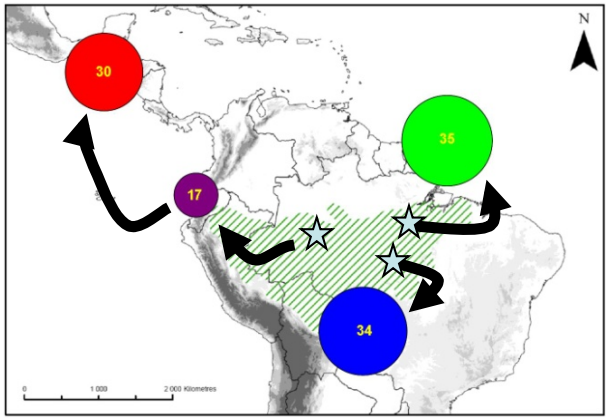


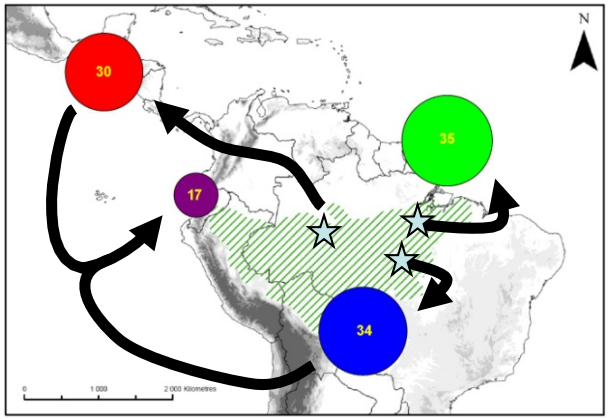


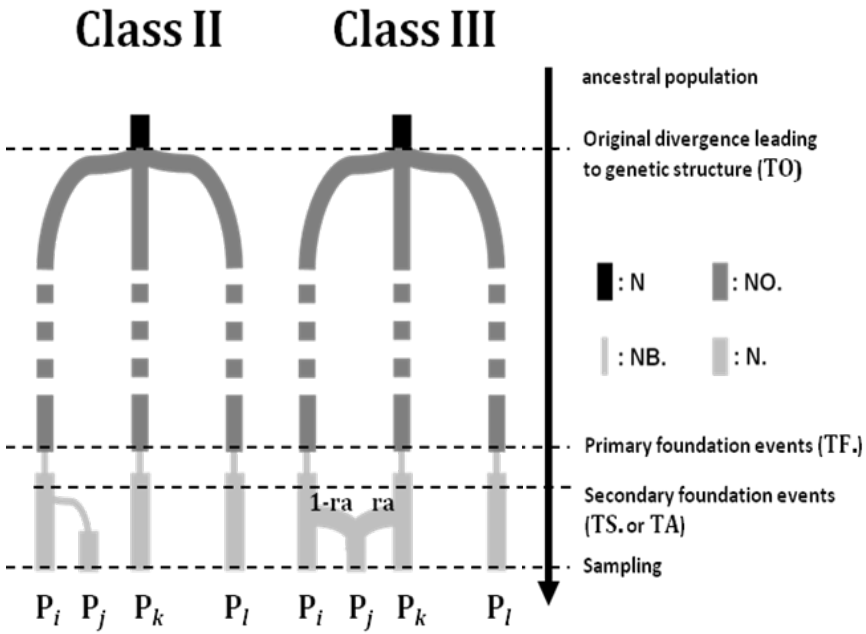


Three independent foundation events

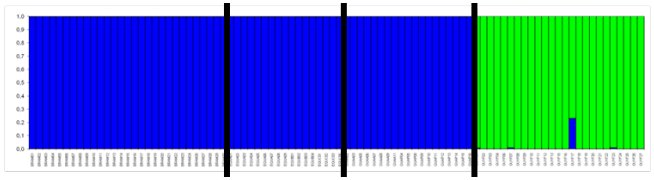


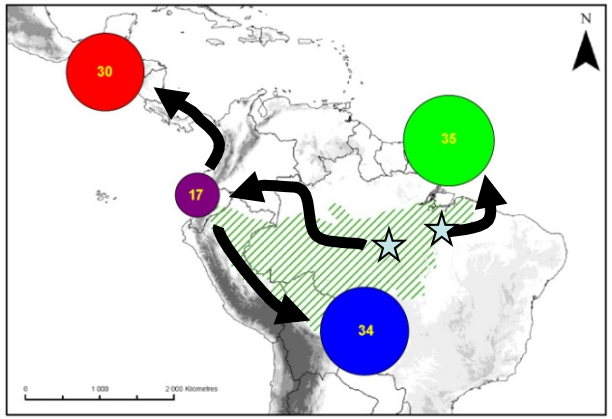


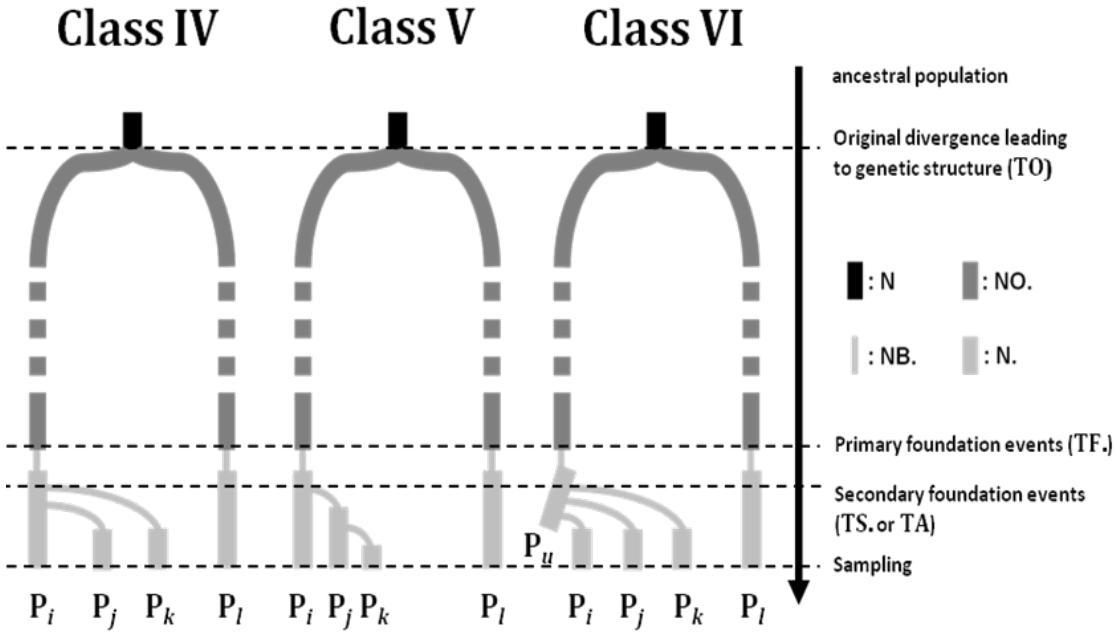


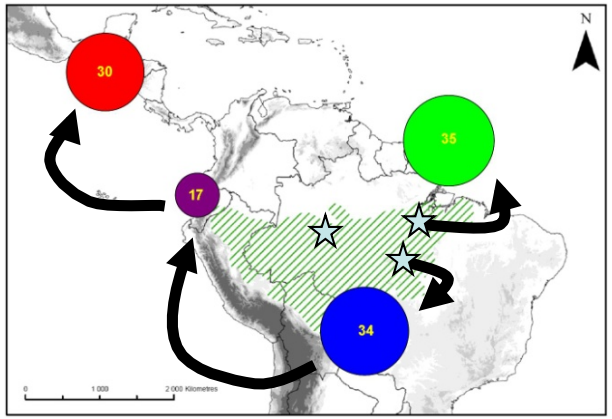


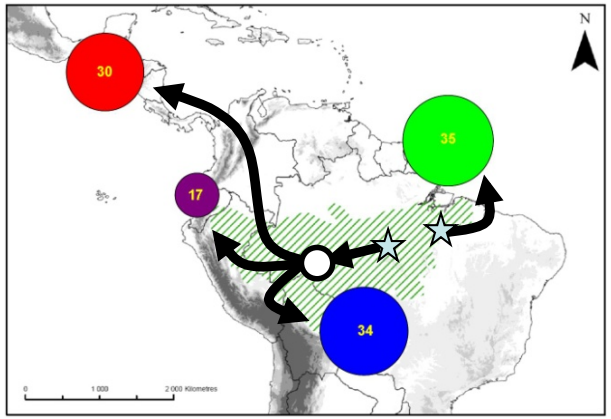
Two independent foundation events



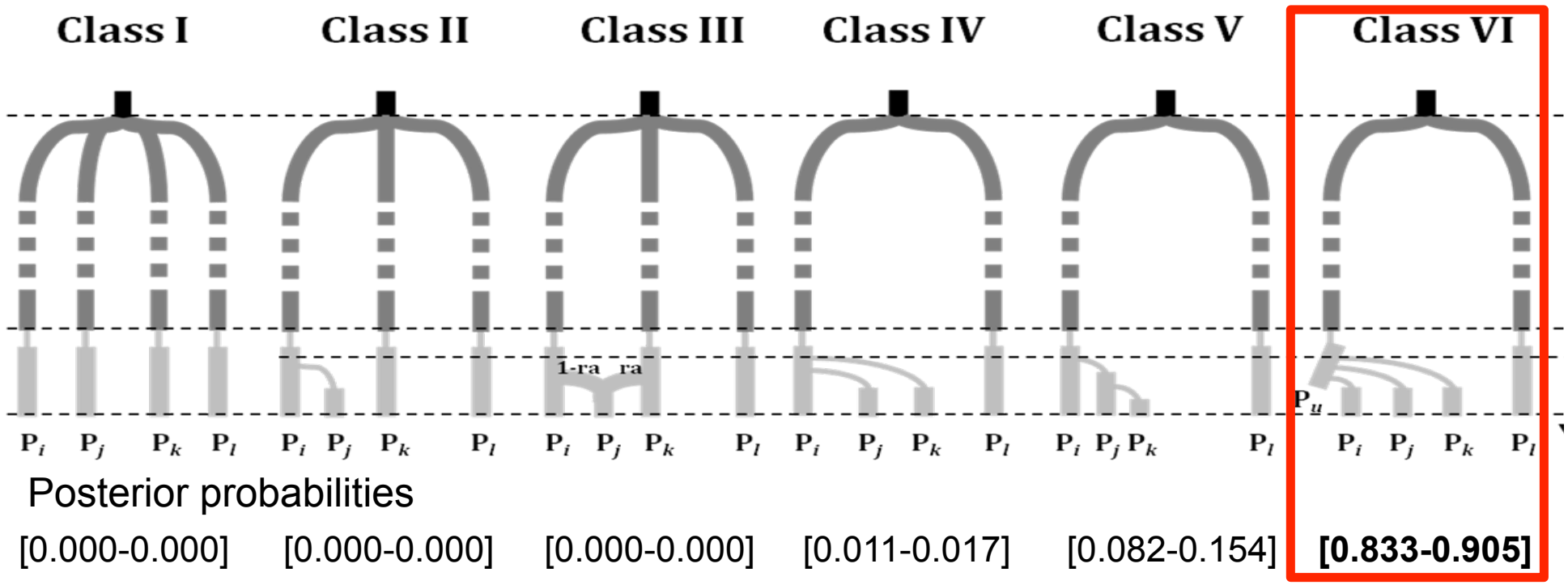








Continental scale dispersal of *Microcyclus ulei*



- Two independent foundation events
- An unknown common origin in western *Hevea* plantations

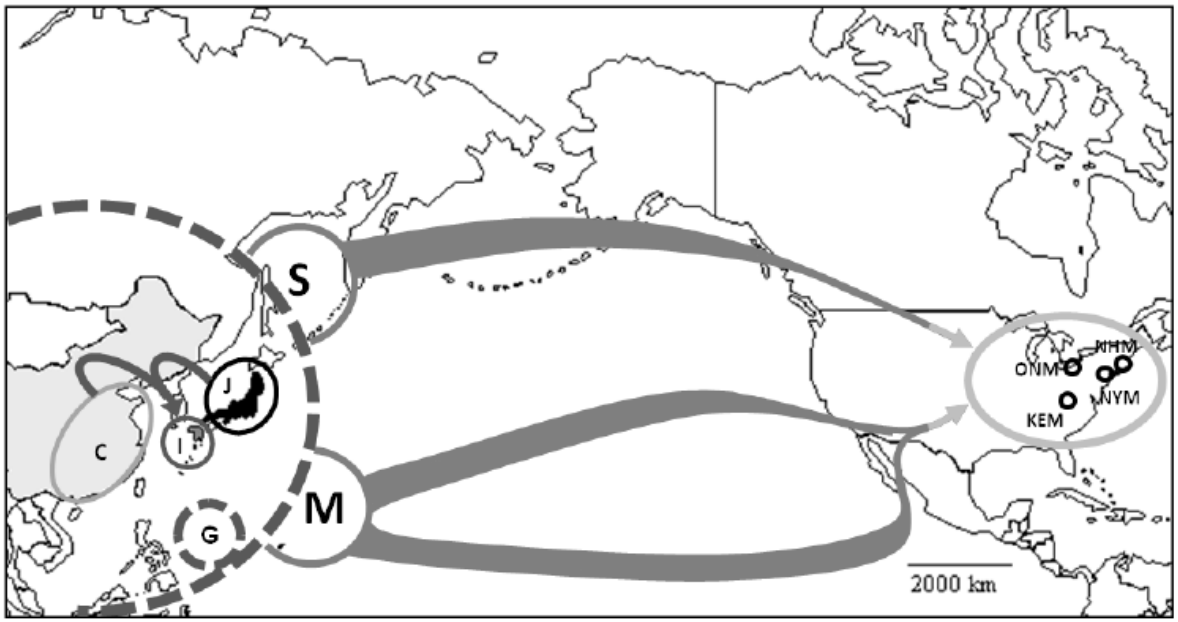
➔ man-mediated dispersal

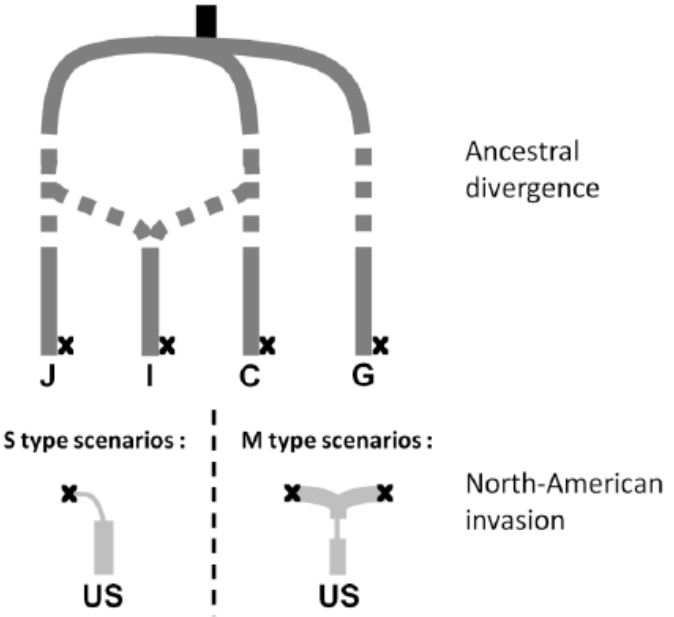
(Barrès *et al.*, submitted)

Introduction of *Cryphonectria parasitica* in North America

Cyril Dutech, Benoit Barrès, Julien Bridier, Cécile Robin, Michael Milgroom and Virginie Ravigné

Introduction of *Cryphonectria parasitica* in North America





-several hypotheses on the introduction in North America exist

-10 scenarios tested (4 with simple and 6 with multiple introduction)

Introduction of *Cryphonectria parasitica* in North America

Posterior probabilities of best tested scenarios :

	Japan	Japan + China	Japan + Intermediate	Japan + Unknown
NYM	**0.34** [0.31-0.38]	0.24 [0.22-0.27]	0.17 [0.15-0.19]	0.21 [0.19-0.24]
KEM	0.03 [0.03-0.04]	0.08 [0.07-0.10]	0.19 [0.17-0.22]	**0.51** [0.47-0.54]
NHM	0.14 [0.12-0.16]	0.14 [0.12-0.16]	0.17 [0.14-0.19]	**0.47** [0.43-0.50]
ONM	0.16 [0.14-0.19]	0.07 [0.06-0.08]	0.22 [0.20-0.25]	**0.39** [0.35-0.42]

- Corroborates the Japanese origin of *C. parasitica*
- No (or undetectable) Chinese introduction
- A possible admixture with an unidentified population

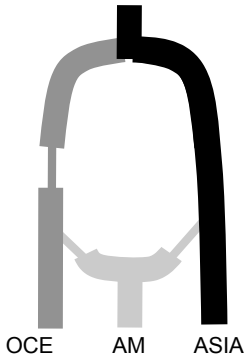
(Dutech *et al.*, accepted)

Introduction of *Mycosphaerella fijiensis* in South America

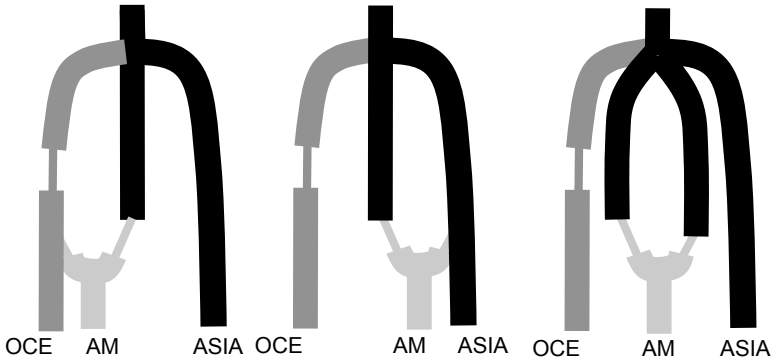
Stéphanie Robert, Jean Carlier, Marie-Françoise Zapater, Catherine Abadie and Virginie Ravigné

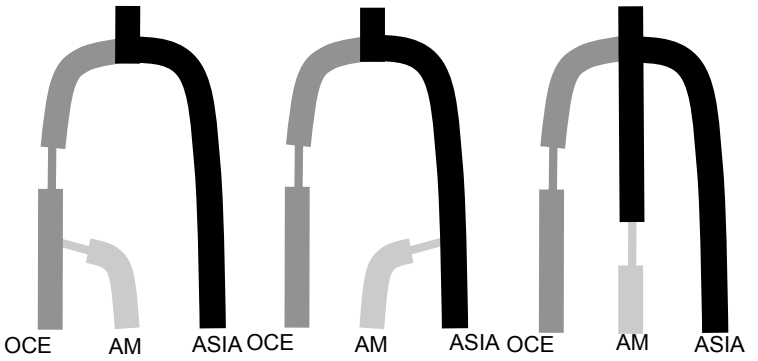
Introduction of *Mycosphaerella fijiensis* in South America

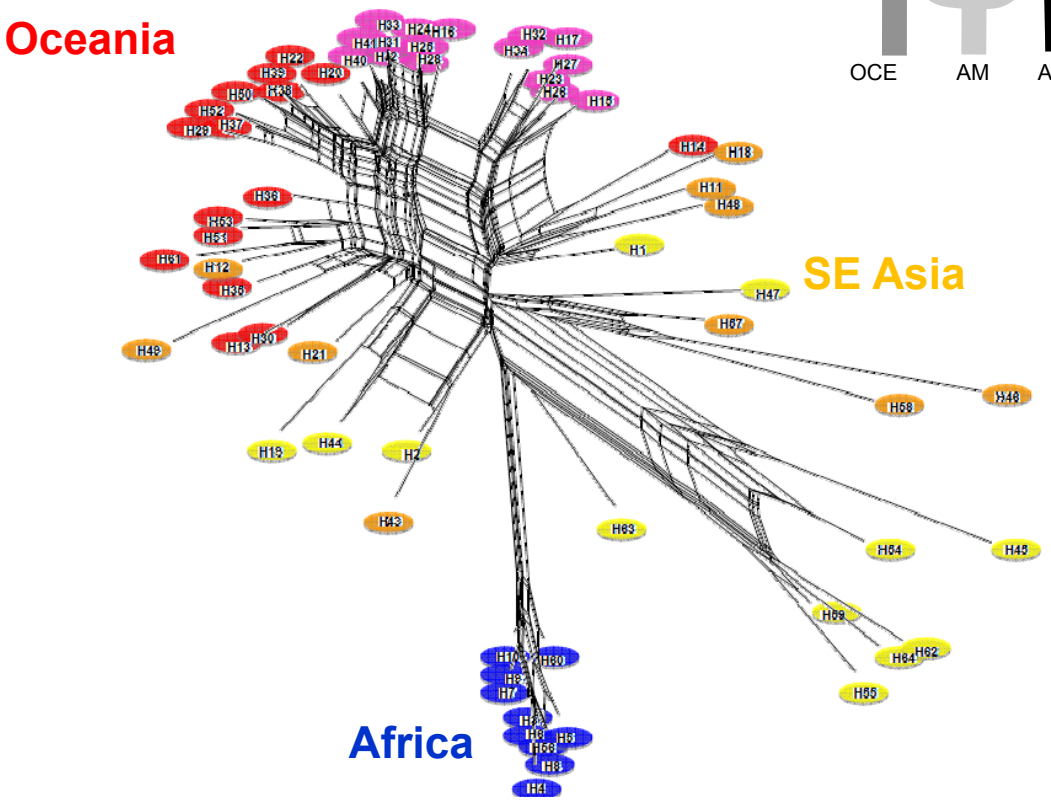
Scenario assumed:



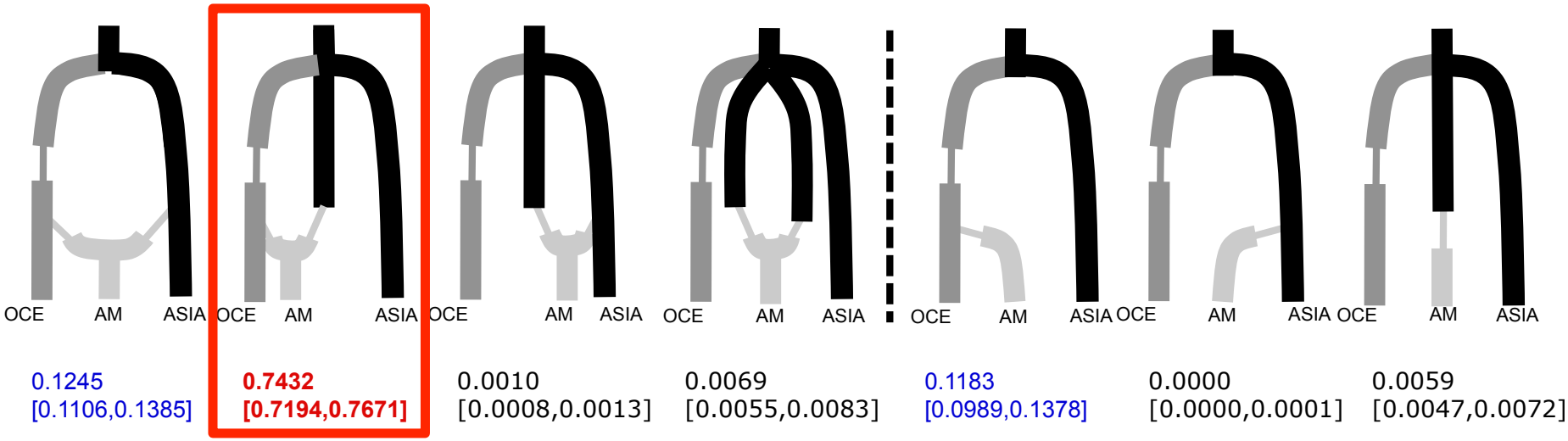
Other possible scenarios:







An introduction with admixture



- Introduction with admixture
- One unidentified source population

Conclusion

Method

ABC is a useful tool to decipher complex colonization scenario

-identification of admixture event

-importance of unsampled population

Biology

-identify source population (confirm or infirm historical knowledge)

-multiple introductions

-underline lack of knowledge on native area of pathogen

Some limitations

-panmictic population
-no regular gene flow between populations
-comparison between tested scenarios only

Thank you for your attention

UMR BIOGECO

Cyril Dutech
Cécile Robin
Julien Bridier

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Jean Carlier
Virginie Ravigné
Elisabeth Fournier
Didier Tharreau
Daniel Bieysse

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Catherine Fenouillet
Christian Cilas
Jean Guyot
Franck Rivano

MICHELIN

Eric Cavaloc
Carlos Mattos
Milton Luiz

UMR DAP

Marc Seguin
Vincent Le Guen

Funding : CIRAD, MICHELIN, ANR EMERFUNDIS, ANR EMILE

Prior distribution of parameters

	Parameter name	distribution	Extremum values
Population effective sizes of the			
ancestral population	N	uniform	{10 – 100,000}
population leading to Brazilian population foundation	NOb	uniform	{10 – 100,000}
population leading to Equatorian population foundation	NOe	uniform	{10 – 100,000}
population leading to Guatemalan population foundation	NOgt	uniform	{10 – 100,000}
population leading to French Guyanian population foundation	NOgy	uniform	{10 – 100,000}
population leading to unsampled population foundation	NOu	uniform	{10 – 100,000}
bottleneck during foundation of Brazilian population	NBb	log-uniform	{1 - 100}
bottleneck during foundation of Equatorian population	NBe	log-uniform	{1 - 100}
bottleneck during foundation of Guatemalan population	NBgt	log-uniform	{1 - 100}
bottleneck during foundation of French Guyana population	NBgy	log-uniform	{1 - 100}
bottleneck during foundation of unsampled population	NBu	log-uniform	{1 - 100}
Brazilian population	Nb	uniform	{10 – 100,000}
Equatorian population	Ne	uniform	{10 – 100,000}
Guatemalan population	Ngt	uniform	{10 – 100,000}
French Guyana population	Ngy	uniform	{10 – 100,000}
Unsampled population	Nu	uniform	{10 – 100,000}
Time of the original divergence leading to genetic structure in source population	TO	uniform	{600 – 100,000}
foundation of the Brazilian population	TFb	log-uniform	{16 - 500}
foundation of the Equatorian population	TFe	log-uniform	{16 - 500}
foundation of the Guatemalan population	TFgt	log-uniform	{16 - 500}
foundation of the French Guyana population	TFgy	log-uniform	{16 - 500}
foundation of the unsampled population	TFu	log-uniform	{16 - 500}
secondary foudation of Brazilian population	TSb	log-uniform	{16 - 500}
secondary foudation of Equatorian population	TSe	log-uniform	{16 - 500}
secondary foudation of Guatemalan population	TSgt	log-uniform	{16 - 500}
secondary foudation of French Guyana population	TSgy	log-uniform	{16 - 500}
admixture event	TA	log-uniform	{16 - 500}

Population effective size :

-population UNIF {10-100,000}
-bottleneck LOG-U {1-100}

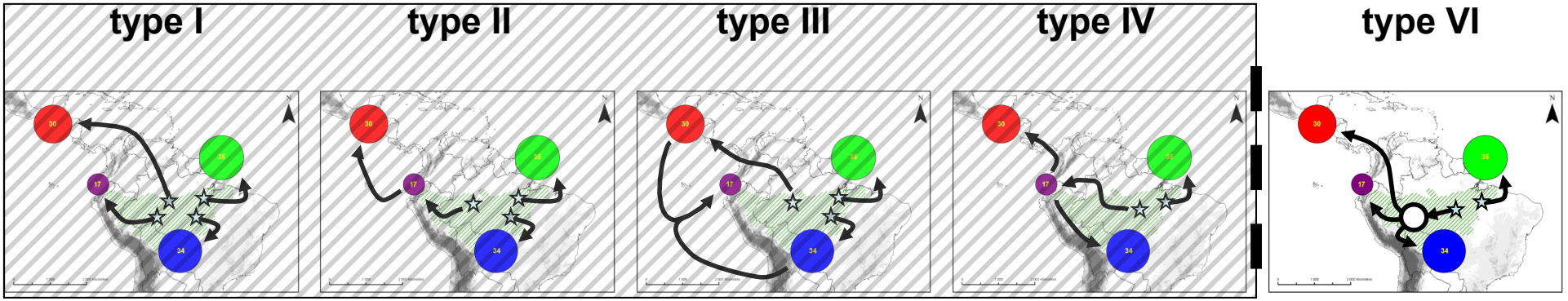
Time of divergence :

-ancestral UNIF {600-100,000}
-foundation pop LOG-U {16-500}

Admixture rate :

- UNIF {0.001-0.999}

The choice of a scenario and its consistency

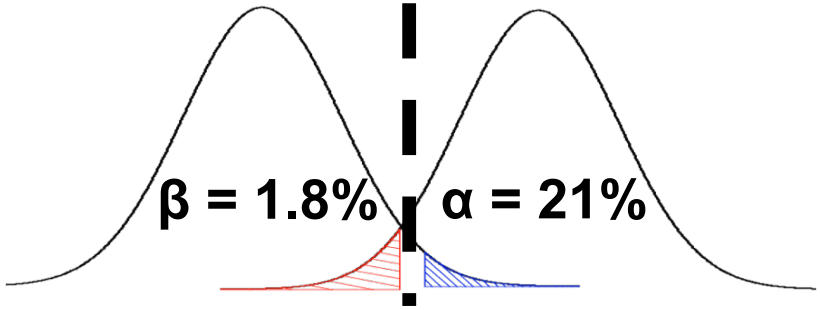


***P*=0.123**
[0.082-0.154]

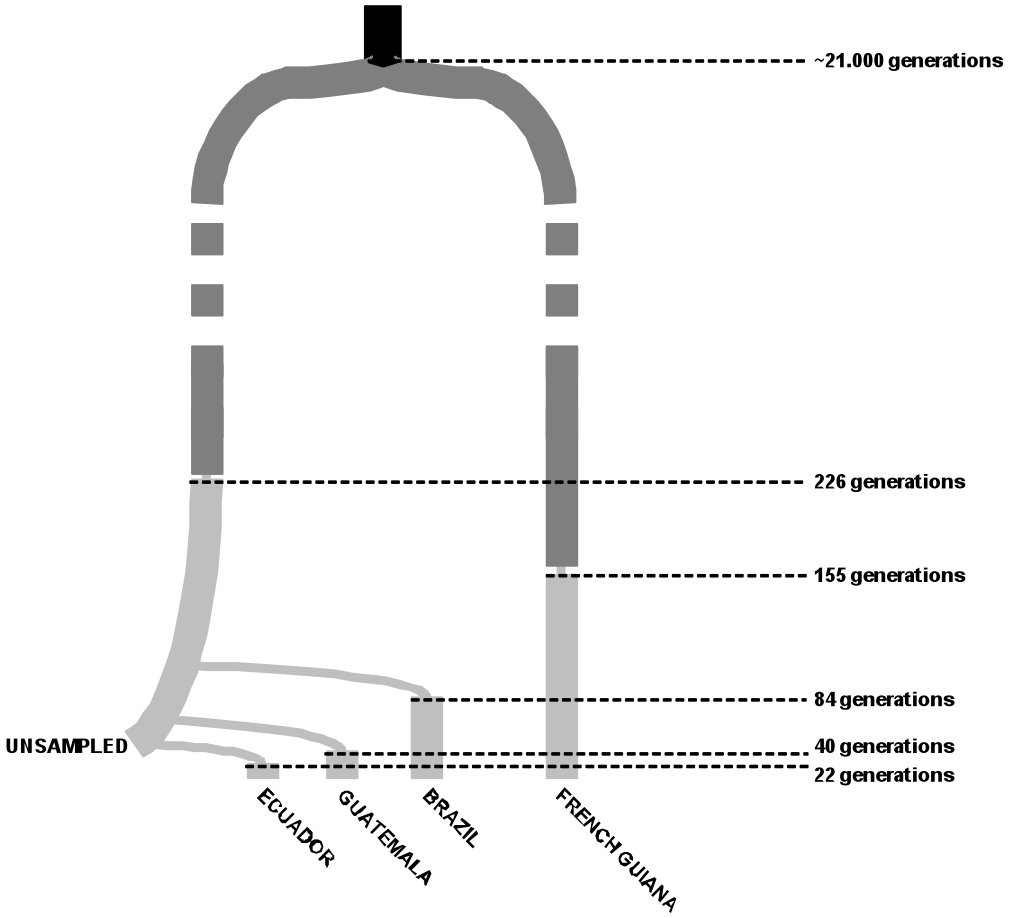
***P*=0.877**
[0.833-0.905]

-Goodness of fit evaluated by Model-checking

-Confidence in the choice of scenario evaluated with pseudo-observed datasets



Final scenario for *M. ulei*

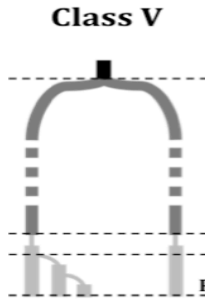


Erreur de Type II = proportion de jeux de données simulés sous de mauvais scénarios et qui pointent vers le meilleur scénario

Ici : 1.8 % !!

Erreur de Type I = proportion de jeux de données simulés sous le bon scénario et qui pointent vers un autre scénario

Ici : 21 % (beurk !)



Toutes les erreurs sont entre ce scénario et le scénario V

Final scenario for *M. fijiensis*